

Amendments to the Claims

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This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1. (currently amended) A method of transcriptional profiling comprising:
subjecting a biological sample to an exogenous stimulation;
measuring transcriptional activity of the biological sample at a first differentiation stage;
measuring transcriptional activity of the biological sample at a second differentiation stage;
and comparing the transcriptional activities from the first and second differentiated stages in at least 5 Mbases, 50 Mbases or 100 Mbases of the genome to obtain a transcription profile, wherein such detection is conducted with probes targeting the 5 Mbases, 50 Mbases or 100 Mbases of the genome at a resolution of 100 bps or less.

Claim 2. (original) The method of claim 1 wherein the measuring comprises obtaining polyA+ enriched cytosolic RNA and hybridizing the RNA to high density oligonucleotide probe arrays.

Claim 3. (original) The method of Claim 2 wherein the oligonucleotide probe array contains at least 100,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

Claim 4. (original) The method of Claim 3 wherein the oligonucleotide probe array contains at least 500,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

Claim 5. (original) The method of Claim 4 wherein the oligonucleotide probe array contains at least 800,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

Claim 6. (original) The method of Claim 5 wherein oligonucleotide array further comprises mismatch (MM) probes, wherein each of the mismatch probes is different from a perfect match (PM) probe in one base.

Claim 7. (original) The method of Claim 6 wherein the mismatch probe is different from the perfect match probe in a middle position.

Claim 8. (original) The method of claim 7 wherein the biological sample is responsive to an exogenous stimulation.

Claim 9. (original) The method of claim 8 wherein the biological sample is a developmentally pluripotent human germ cell tumor-derived cell line.

Claim 10. (new) The method of claim 1 wherein the resolution is at 30 bps or less.

Claim 11. (new) The method of claim 1 wherein the resolution is at 10 bps or less.

Claim 12. (new) The method of claim 1 wherein the resolution is at 1 bps.